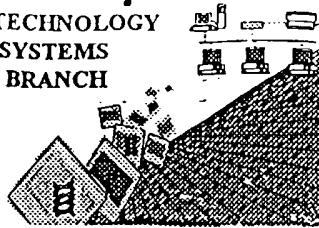# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/816,571_

Source: _PFWO_

Date Processed by STIC: _4/8/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER:

SERIAL NUMBER: *10/816,591*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics **Wrapped Aminos** — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino **Numbering** — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 **"bug"** — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences **(OLD RULES)** — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences **(NEW RULES)** — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's **(NEW RULES)** — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> **Response** — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 **"bug"** — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 04/08/2004
PATENT APPLICATION: **US/10/816,591**   TIME: 10:13:52

Input Set : **A:\NHL-NP-46 Sequence Listing.txt**
Output Set: **N:\CRF4\04082004\J816591.raw**

```
   3 <110> APPLICANT: Fuertes-Lopez, Laura        ,
   4        Timon-Jimenez, Marcos
   6 <120> TITLE OF INVENTION: DNA EXPRESSION CONSTRUCT FOR TREATMENT OF INFECTIONS WITH
   7        LEISHMANIASIS
   9 <130> FILE REFERENCE: NHL-NP-46
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/816,591
C--> 11 <141> CURRENT FILING DATE: 2004-04-01
  11 <150> PRIOR APPLICATION NUMBER: DE 101 48 732.0
  12 <151> PRIOR FILING DATE: 2001-10-02
 .14 <150> PRIOR APPLICATION NUMBER: DE 101 56 679.4
  15 <151> PRIOR FILING DATE: 2001-11-12
  17 <150> PRIOR APPLICATION NUMBER: PCT/DE02/03799
  18 <151> PRIOR FILING DATE: 2002-10-02
  20 <160> NUMBER OF SEQ ID NOS: 9
  22 <170> SOFTWARE: PatentIn version 3.2
  24 <210> SEQ ID NO: 1
  25 <211> LENGTH: 4791
  26 <212> TYPE: DNA
  27 <213> ORGANISM: Plasmid pSCp36
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  33 <223> OTHER INFORMATION: Kanamycin resistance, reverse complementary
  35 <220> FEATURE:
  36 <221> NAME/KEY: promoter
  37 <222> LOCATION: (2447)..(3243)
  38 <223> OTHER INFORMATION: CMV
  40 <220> FEATURE:
  41 <221> NAME/KEY: Intron
  42 <222> LOCATION: (3250)..(3386)
  44 <220> FEATURE:
  45 <221> NAME/KEY: misc_feature
  46 <222> LOCATION: (3393)..(4331)
  47 <223> OTHER INFORMATION: p36 protein
  49 <220> FEATURE:
  50 <221> NAME/KEY: polyA_site
  51 <222> LOCATION: (4338)..(4539)
  52 <223> OTHER INFORMATION: poly A site aus SV 40
  54 <400> SEQUENCE: 1
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  57 tcagctcact caaaggcggt aatacggtta tccacagaat caggggataa cgcaggaaag    120
  59 aacatgtctc gggaggcctc acgtgacatg tgagcaaaag gccagcaaaa ggccaggaac    180
  61 cgtaaaaagg ccgcgttgct ggcgtttttc cataggctcc gcccccctga cgagcatcac    240
```

Does Not Comply
Corrected Diskette Needed
CP5.3 -4)

RAW SEQUENCE LISTING   DATE: 04/08/2004
PATENT APPLICATION: US/10/816,591   TIME: 10:13:52

Input Set : A:\NHL-NP-46 Sequence Listing.txt
Output Set: N:\CRF4\04082004\J816591.raw

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 67 ctgtccgcct ttctcccttc gggaagcgtg gcgctttctc atagctcacg ctgtaggtat    420
 69 ctcagttcgg tgtaggtcgt tcgctccaag ctgggctgtg tgcacgaacc ccccgttcag    480
 71 cccgaccgct gcgccttatc cggtaactat cgtcttgagt ccaacccggt aagacacgac    540
 73 ttatcgccac tggcagcagc cactggtaac aggattagca gagcgaggta tgtaggcggt    600
 75 gctacagagt tcttgaagtg gtggcctaac tacggctaca ctagaaggac agtatttggt    660
 77 atctgcgctc tgctgaagcc agttaccttc ggaaaaagag ttggtagctc ttgatccggc    720
 79 aaacaaacca ccgctggtag cggtggtttt tttgtttgca agcagcagat tacgcgcaga    780
 81 aaaaaaggat ctcaagaaga tcctttgatc ttttctacgg ggtctgacgc tcagtggaac    840
 83 gaaaactcac gttaagggat tttggtcatg agattatcaa aaaggatctt cacctagatc    900
 85 cttttaaatt aaaaatgaag ttttaaatca atctaaagta tatatgagta aacttggtct    960
 87 gacagttacc aatgcttaat cagtgaggca cctatctcag cgatctgtct atttcgttca   1020
 89 tccatagttg cctgactccc cgtctcagaa gaactcgtca agaaggcgat agaaggcgat   1080
 91 gcgctgcgaa tcgggagcgg cgataccgta aagcacgagg aagcggtcag cccattcgcc   1140
 93 gccaagctct tcagcaatat cacgggtagc caacgctatg tcctgatagc ggtccgccac   1200
 95 acccagccgg ccacagtcga tgaatccaga aaagcggcca ttttccacca tgatattcgg   1260
 97 caagcaggca tcgccatggg tcacgacgag atcctcgccg tcgggcatgc tcgccttgag   1320
 99 cctggcgaac agttcggctg gcgcgagccc ctgatgctct tcgtccagat catcctgatc   1380
101 gacaagaccg gcttccatcc gagtacgtgc tcgctcgatg cgatgtttcg cttggtggtc   1440
103 gaatgggcag gtagccggat caagcgtatg cagccgccgc attgcatcag ccatgatgga   1500
105 tactttctcg gcaggagcaa ggtgagatga caggagatcc tgccccggca cttcgcccaa   1560
107 tagcagccag tcccttcccg cttcagtgac aacgtcgagc acagctgcgc aaggaacgcc   1620
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125 cggatgccgg gagcagacaa gcccgtcagg gcgcgtcagc gggtgttggc gggtgtcggg   2160
127 gctggcttaa ctatgcggca tcagagcaga ttgtactgag agtgcaccat atgcggtgtg   2220
129 aaataccgca cagatgcgta aggagaaaat accgcatcag cgccattcg ccattcaggc    2280
131 tgcgcaactg ttgggaaggg cgatcggtgc gggcctcttc gctattacgc cagctggcga   2340
133 aagggggatg tgctgcaagg cgattaagtt gggtaacgcc agggttttcc cagtcacgac   2400
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151 cctggcatta tgcccagtac atgaccttac gggactttcc tacttggcag tacatctacg   2940
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155 agcggtttga ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt   3060
157 tttggcacca aaatcaacgg gactttccaa aatgtcgtaa taaccccgcc ccgttgacgc   3120
159 aaatgggcgg taggcgtgta cggtgggagg tctatataag cagaggtcgt ttagtgaacc   3180
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RAW SEQUENCE LISTING   DATE: 04/08/2004
PATENT APPLICATION: **US/10/816,591**   TIME: 10:13:52

Input Set : **A:\NHL-NP-46 Sequence Listing.txt**
Output Set: **N:\CRF4\04082004\J816591.raw**

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161 gtcagatcac tagaagcttt attgcggtag tttatcacag ttaaattgct aacgcagtca 3240
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165 ggcttgtcga gacagagaag actcttgcgt ttctgatagg cacctattgg tcttactgac 3360
167 atccactttg cctttctctc cacaggggta ccatgaacta cgagggtcac ctgaagggcc 3420
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201 gctttatttg tgaaatttgt gatgctattg ctttatttgt aaccattata agctgcaata 4440
203 aacaagttaa caacaacaat tgcattcatt ttatgtttca ggttcagggg gaggtgtggg 4500
205 aggttttta aagcaagtaa aacctctaca aatgtggtag aattcagggg gagacccaat 4560
207 tcgtaatcat ggtcatagct gtttcctgtg tgaaattgtt atccgctcac aattccacac 4620
209 aacatacgag ccggaagcat aaagtgtaaa gcctggggtg cctaatgagt gagctaactc 4680
211 acattaattg cgttgcgctc actgcccgct ttccagtcgg gaaacctgtc gtgccagctg 4740
213 cattaatgaa tcggccaacg cgcggggaga ggcggtttgc gtattgggcg c 4791
216 <210> SEQ ID NO: 2
217 <211> LENGTH: 11
218 <212> TYPE: PRT
219 <213> ORGANISM: Human immunodeficiency virus type 1, TAT peptide
221 <400> SEQUENCE: 2
223 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
224 1               5                   10
227 <210> SEQ ID NO: 3
228 <211> LENGTH: 7
229 <212> TYPE: PRT
230 <213> ORGANISM: Simian virus 40, NLS peptide
232 <400> SEQUENCE: 3
234 Pro Lys Lys Lys Arg Lys Val
235 1               5
238 <210> SEQ ID NO: 4
239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: ODN 1
244 <220> FEATURE:
245 <221> NAME/KEY: modified_base
246 <222> LOCATION: (12)..(12)
247 <223> OTHER INFORMATION: xT = Thymin modified with a reactive amino group
```

[Handwritten annotations:]

— Invalid Response (circling "ODN 1")

mandatory, <213> Response has to be either Artificial Unknown on Genus/Species.

Please see item #10 on error Summary Sheet.

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249 <400> SEQUENCE: 4
250 gggagtccag ttttctggac
253 <210> SEQ ID NO: 5
254 <211> LENGTH: 20
255 <212> TYPE: DNA
256 <213> ORGANISM: ODN 2
258 <400> SEQUENCE: 5
259 aggggtccag ttttctggac
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 33
264 <212> TYPE: DNA
265 <213> ORGANISM: 1. PCR: Primer left
267 <400> SEQUENCE: 6
268 ttatatggta ccatgaacat acgagggtca cct
271 <210> SEQ ID NO: 7
272 <211> LENGTH: 42
273 <212> TYPE: DNA
274 <213> ORGANISM: 1. PCR: Primer right
276 <400> SEQUENCE: 7
277 ttatatgagc tcagaagaca cggacaggga cctcttccgt cg
280 <210> SEQ ID NO: 8
281 <211> LENGTH: 33
282 <212> TYPE: DNA
283 <213> ORGANISM: 2. PCR: Primer left
285 <400> SEQUENCE: 8
286 ttatatggta ccatgaacat acgagggtca cct
289 <210> SEQ ID NO: 9
290 <211> LENGTH: 33
291 <212> TYPE: DNA
292 <213> ORGANISM: 2. PCR: Primer right
294 <400> SEQUENCE: 9
295 ttatatgagc tcttactcgg ccgtcggaga tgg
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(handwritten annotations:) Same errors 20

See item 20
#10
on error
Summary 42
Sheet

20
33
42
33
33

VERIFICATION SUMMARY   DATE: 04/08/2004
PATENT APPLICATION: **US/10/816,591**   TIME: 10:13:53

Input Set : **A:\NHL-NP-46 Sequence Listing.txt**
Output Set: **N:\CRF4\04082004\J816591.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date